

Form PTO 1390 (REV 5-93)		U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE	ATTORNEY'S DOCKET NUMBER P50593
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED / ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371			U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.5) 09/308397
INTERNATIONAL APPLICATION NO. PCT/US97/20992	INTERNATIONAL FILING DATE 14 November 1997	PRIORITY DATE CLAIMED 18 November 1996	
TITLE OF INVENTION Novel FabD			
APPLICANT(S) FOR DO/EO/US Daniel R Gentry, John T Lonsdale, David J Payne, Stewart C Pearson, Glenn Van Aller			

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☒ An Information Disclosure Statement under 37 C.F.R. 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. 3.28 and 3.31 is included.
13. ☐ A FIRST preliminary amendment.
☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☐ Other items or information:

09/308397-051899

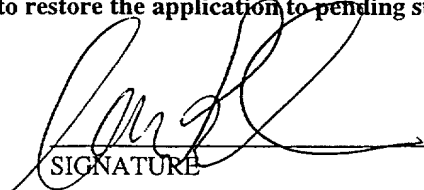
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US APPLICATION NO. (if known see 37 CFR 1.50) Unknown		INTERNATIONAL APPLICATION NO. PCT/US97/20992		ATTORNEYS DOCKET NO. P50593	
17. [X] The following fees are submitted:				CALCULATIONS PTO USE ONLY	
Basic National Fee (37 C.F.R. 1.492(a)(1)-(5)):					
Search Report has been prepared by the EPO or JPO\$930.00					
International Preliminary Examination Fee paid to USPTO (37 CFR 1.482)\$720.00					
No International Preliminary Examination Fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2))\$790.00					
Neither International Preliminary Examination Fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO.....\$1070.00					
International Preliminary Examination Fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4).....\$98.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$98.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than o 20 o 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$0.00	
Claims	Number Filed	Number Extra	Rate		
Total claims	24 - 20 =	4	4x \$22.00	\$88.00	
Independent claims	7 - 3 =	4	4 x \$82.00	\$328.00	
Multiple dependent claims (if applicable)		0	+ \$270.00	\$0.00	
TOTAL OF ABOVE CALCULATIONS =				\$514.00	
Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28).				\$	
SUBTOTAL =				\$514.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)) +				\$	
TOTAL NATIONAL FEE =				\$514.00	
				Amount to be refunded	\$
				charged	\$

- a. ☐ A check in the amount of \$_____ to cover the above fees is enclosed.
- b. ☒ Please charge my Deposit Account No. 19-2570 in the amount of **\$514.00** to cover the above fees.
A duplicate copy of this sheet is enclosed.
- c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 19-2570. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

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09/308397

Novel FabD**FIELD OF THE INVENTION**

This invention relates to newly identified polynucleotides and polypeptides, and their production and uses, as well as their variants, agonists and antagonists, and their uses. In particular, the invention relates to novel polynucleotides and polypeptides of the malonyl-CoA:ACP family, hereinafter referred to as "FabD".

BACKGROUND OF THE INVENTION

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain. It is particularly preferred to employ Streptococcal genes and gene products as targets for the development of antibiotics.

The frequency of *Streptococcus pneumoniae* infections has risen dramatically in the past few decades. This has been attributed to the emergence of multiply antibiotic resistant strains and an increasing population of people with weakened immune systems. It is no longer uncommon to isolate *Streptococcus pneumoniae* strains which are resistant to some or all of the standard antibiotics. This phenomenon has created a demand for both new anti-microbial agents, vaccines, and diagnostic tests for this organism.

The pathway for the biosynthesis of saturated fatty acids is very similar in prokaryotes and eukaryotes. However, whilst the chemical reactions may not vary, the organisation of the biosynthetic apparatus is very different. Vertebrates and yeasts possess type I fatty acid synthases (FASs) in which all of the enzymatic activities are encoded on one or two polypeptide chains, respectively. The acyl carrier protein (ACP) is an integral part of the complex. In contrast, in most bacterial and plant FASs (type II) each of the reactions are catalysed by distinct monofunctional enzymes and the ACP is a discrete protein.

Mycobacteria are unique in that they possess both type I and II FASs; the former is involved in basic fatty acid biosynthesis whereas the latter is involved in synthesis of complex cell envelope lipids such as mycolic acids. There therefore appears to be

considerable potential for selective inhibition of the bacterial systems by broad spectrum antibacterial agents (Rock, C. & Cronan, J. 1996. *Biochimica et Biophysica Acta* 1302, 1-16; Jackowski, S. 1992. In *Emerging Targets in Antibacterial and Antifungal Chemotherapy*. Ed. J. Sutcliffe & N. Georgopapadakou. Chapman & Hall, New York;

5 Jackowski, S. *et al.* (1989). *J. Biol. Chem.* 264, 7624-7629.)

The first step in the biosynthetic cycle is the condensation of malonyl-ACP with acetyl-CoA by FabH. Prior to this, malonyl-ACP is synthesised from ACP and malonyl-CoA by FabD, malonyl CoA:ACP transacylase. In subsequent rounds malonyl-ACP is condensed with the growing-chain acyl-ACP (FabB and FabF, synthases I and II
10 respectively). The second step in the elongation cycle is ketoester reduction by NADPH-dependent β -ketoacyl-ACP reductase (FabG). Subsequent dehydration by β -hydroxyacyl-ACP dehydrase (either FabA or FabZ) leads to trans-2-enoyl-ACP which is in turn converted to acyl-ACP by NADH-dependent enoyl-ACP reductase (FabI). Further rounds of this cycle, adding two carbon atoms per cycle, eventually lead to palmitoyl-ACP
15 whereupon the cycle is stopped largely due to feedback inhibition of FabH and I by palmitoyl-ACP (Heath, et al, (1996), *J.Biol.Chem.* 271, 1833-1836).

Cerulenin and thiolactomycin are potent and selective inhibitors of bacterial fatty acid biosynthesis. Extensive work with these inhibitors in Gram-negative bacteria has proved that this biosynthetic pathway is essential for viability. Little work has been carried
20 out in Gram-positive bacteria. No mutants totally lacking FabD activity have been described. No mammalian homologues to FabD have yet been identified. No marketed antibiotics are targeted against fatty acid biosynthesis, therefore it is unlikely that novel antibiotics would be rendered inactive by known antibiotic resistance mechanisms

Clearly, there exists a need for factors, such as the FabD embodiments of the invention, that have a present benefit of being useful to screen compounds for antibiotic
25 activity. Such factors are also useful to determine their role in pathogenesis of infection, dysfunction and disease. There is also a need for identification and characterization of such factors and their antagonists and agonists to find ways to prevent, ameliorate or correct such infection, dysfunction and disease.

30 Certain of the polypeptides of the invention possess amino acid sequence homology to a known proteins.

There is clearly an unmet need for developing new classes of antibiotic compounds. Clearly, there is a need for factors that may be used to screen compounds for antibiotic

activity and which may also be used to determine their roles in pathogenesis of infection, dysfunction and disease. There is a need, therefore, for identification and characterization of such factors which can play a role in preventing, ameliorating or correcting infections, dysfunctions or diseases.

- 5 The polypeptide of the present invention has the conserved residues, and have amino acid sequence homology to known transacylase protein.

SUMMARY OF THE INVENTION

- It is an object of the invention to provide polypeptides that have been identified as novel FabD polypeptides by homology between the amino acid sequence set out in Table 1
10 [SEQ ID NO: 2 or 4] and a known amino acid sequence or sequences of other proteins such as FabD protein.

 It is a further object of the invention to provide polynucleotides that encode FabD polypeptides, particularly polynucleotides that encode the polypeptide herein designated FabD.

- 15 In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding FabD polypeptides comprising a sequence set out in Table 1 [SEQ ID NO:1 or 3 or 5] which includes a full length gene, or a variant thereof.

- In another particularly preferred embodiment of the invention there is a novel FabD protein from *Streptococcus pneumoniae* comprising the amino acid sequence of Table 1
20 [SEQ ID NO:2 or 4 or 6], or a variant thereof.

 In accordance with another aspect of the invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Streptococcus pneumoniae* 0100993 strain contained in the deposited strain.

- A further aspect of the invention there are provided isolated nucleic acid molecules
25 encoding FabD, particularly *Streptococcus pneumoniae* FabD, including mRNAs, cDNAs, genomic DNAs. Further embodiments of the invention include biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

- In accordance with another aspect of the invention, there is provided the use of a
30 polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants of FabD and polypeptides encoded thereby.

Another aspect of the invention there are provided novel polypeptides of *Streptococcus pneumoniae* referred to herein as FabD as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

5 Among the particularly preferred embodiments of the invention are variants of FabD polypeptide encoded by naturally occurring alleles of the FabD gene.

In a preferred embodiment of the invention there are provided methods for producing the aforementioned FabD polypeptides.

10 In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing FabD expression, treating disease, assaying genetic variation, and administering a FabD polypeptide or polynucleotide to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

15 In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to FabD polynucleotide sequences, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against FabD polypeptides.

20 In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit
25 binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and
30 activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided FabD agonists and antagonists, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a FabD polynucleotide or a FabD polypeptide for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

DESCRIPTION OF THE INVENTION

The invention relates to novel FabD polypeptides and polynucleotides as described in greater detail below. In particular, the invention relates to polypeptides and polynucleotides of a novel FabD of *Streptococcus pneumoniae*, which is related by amino acid sequence homology to FabD polypeptide of a different species. The invention relates especially to FabD having the nucleotide and amino acid sequences set out in Table 1 as SEQ ID NO: 1 and SEQ ID NO: 2 respectively, and to the FabD nucleotide sequences of the DNA in the deposited strain and amino acid sequences encoded thereby.

TABLE 1

FabD Polynucleotide and Polypeptide Sequences

(A) Sequences from *Streptococcus pneumoniae* FabD polynucleotide sequence [SEQ ID NO:1].

5' -ATGACTAAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG
GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC
GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT
ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC
TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC
GGCGCCTTGGATTTTGAAGATGCGGTTGCCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA
GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC
ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC
ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT
TTGCAAGAAGCAGGTGCCAAACGCTTGATTCTCTTAAGGTGTCAGGTCCCTTTTCACACC
GCTCTCCTTGAGCCTGCTAGCCAGAACTAGCTGAACTCTAGCTCAGGTAAGTTTTTCA
GATTTTACTTGTCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT
GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTTCGTTTCTATGAAAGTATTGGGGTC
ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTACAGT

TTTGTTAAAAAATTGATCAAAC TGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA
GTAGCACTTTTAGAAAAATAG-3'

- (B) *Streptococcus pneumoniae* FabD polypeptide sequence deduced from the
5 polynucleotide sequence in this table [SEQ ID NO:2].

NH₂-MTKTAFLFAGQGAQYLGMRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY
TQPAILATSVAIYRLLQEKGYQPD MVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME
EAAPADSGKMAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL
LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTAAVMQKEDI
10 AQLLTRQVKPEVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVALLEK-
COOH

- (C) Polynucleotide sequences comprising *Streptococcus pneumoniae* FabD ORF
sequence [SEQ ID NO:3]. N-terminal coding region of a fabD embodiment. The open
15 reading frame starts at nucleotide position 85.

5'-1 CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA
51 GAAGAAGCCT CTCGCTGGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT
101 TTTTATTTGC TGGTCAAGGT GCCCAGTATC TAGGGATGGG ACGGGATTTC
151 TATGATCAGT ATCCGATTGT CAAAGAAACG ATTGATCGAG CGAGTCAGGT
20 201 GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA GACAAACTCA
251 ATCAGACCCG CTATACGCAA CCAGCCATTC TAGCGACTTC GGTGCTATC
301 TACCGTTTAT TGCAAGAAAA GGGCTATCAG CCTGATATGG TTGCTGGTTT
351 GTCTCTTGGA GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTTTG
401 AAGATGCGGT TGCCTTGGTA GCTAAGCGTG GAGCCTATAT GGAAGAAGCG-3'

- 25 (D) Polynucleotide sequences comprising *Streptococcus pneumoniae* FabD ORF
sequence [SEQ ID NO:5]. C-terminal coding region of fabD embodiment. The open
reading frame starts at nucleotide position 2.

5'-1 TGCTGAACTT GGCAAGATGG TAGCAGTTCT CAATACGCCA GTAGAGGTCA
30 51 TTGAAGAAGC CTGTCAAAAG CTTCTGGAAC TTGGAGTGGT TACTCCAGCC
101 AACTATAACA CACCTGCACA AATCGTCATT GCTGGAGAAG TGGTTGCAGT
151 TGATCGAGCG GTTGAACTTT TGCAAGAAGC AGGTGCCAAA CGCTTGATTCT
201 CTCTTAAGGT GTCAGGTCCC TTTCACACCG CTCTCCTTGA GCCTGCTAGC
251 CAGAAACTAG CTGAAACTCT AGCTCAGGTA AGTTTTTCAG ATTTTACTTG
35 301 TCCCCTAGTC GGCAATACAG AAGCTGCTGT GATGCAAAAA GAGGACATTG
351 CTCAGCTCTT GACGCGTCAG GTCAAGGAAC CCGTTCGTTT CTATGAAAGT

401 ATTGGGGTCA TGCAAGAAGC AGGCATAAGC AACTTATTCG AGATTGGACC
 451 GGGGAAAGTC TTGTCAGGTT TTGTTAAAAA AATTGATCAA ACTGCTCACT
 501 TAGCTCATGT GGAAGATCAA GCGAGTTTAG TAGCACTTTT AGAAAAA -3'

- 5 (E) *Streptococcus pneumoniae* FabD polypeptide sequence deduced from the polynucleotide ORF sequence in this table [SEQ ID NO:4]. N-terminus of a fabD polypeptide embodiment.

NH₂-1 MTKTAFLFAG QGAQYLGMR DFYDQYPIVK ETIDRASQVL GYDLRYLIDT

51 EEDKLNQTRY TQPAILATSV AIYRLLQKEG YQPDVMAGLS LGEYSALVAS

- 10 101 GALDFEDAVA LVAKRGAYME EA-COOH

- (F) *Streptococcus pneumoniae* FabD polypeptide sequence deduced from the polynucleotide ORF sequence in this table [SEQ ID NO:6].

A fabD polypeptide sequence embodiment comprising a putative C-terminus.

15

NH₂-1 AELGKMVAVL NTPVEVIEEA CQKLELGVV TPANYNTPAQ IVIAGEVVAV

51 DRAVELLQEA GAKRLIPLKV SGPFTALLE PASQKLAETL AQVSFSDFTC

101 PLVGNTAAV MQKEDIAQLL TRQVKEPVRF YESIGVMQEA GISNLFIEIGP

151 GKVLSGFVKK IDQTAHLAHV EDQASLVALL EK-COOH'

20

Deposited materials

A deposit containing a *Streptococcus pneumoniae* 0100993 strain has been deposited with the National Collections of Industrial and Marine Bacteria Ltd. (herein "NCIMB"), 23 St. Machar Drive, Aberdeen AB2 1RY, Scotland on 11 April 1996 and assigned deposit number 40794. The deposit was described as *Streptococcus pneumoniae* 0100993 on deposit.

25

On 17 April 1996 a *Streptococcus pneumoniae* 0100993 DNA library in *E. coli* was similarly deposited with the NCIMB and assigned deposit number 40800. The *Streptococcus pneumoniae* strain deposit is referred to herein as "the deposited strain" or as "the DNA of the deposited strain."

30

The deposited strain contains the full length FabD gene. The sequence of the polynucleotides contained in the deposited strain, as well as the amino acid sequence of the polypeptide encoded thereby, are controlling in the event of any conflict with any description of sequences herein.

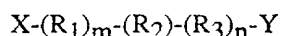
The deposit of the deposited strain has been made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for Purposes of Patent Procedure. The strain will be irrevocably and without restriction or condition released to the public upon the issuance of a patent. The deposited strain is provided merely as
 5 convenience to those of skill in the art and is not an admission that a deposit is required for enablement, such as that required under 35 U.S.C. §112.

A license may be required to make, use or sell the deposited strain, and compounds derived therefrom, and no such license is hereby granted.

Polypeptides

10 The polypeptides of the invention include a polypeptide of Table 1 [SEQ ID NO:2 or 4 or 6] (in particular the mature polypeptide) as well as polypeptides and fragments, particularly those which have the biological activity of FabD, and also those which have at least 70% identity to a polypeptide of Table 1 [SEQ ID NO:1 or 3 or 5] or the relevant portion, preferably at least 80% identity to a polypeptide of Table 1 [SEQ ID NO:2 or 4] and more
 15 preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide of Table 1 [SEQ ID NO:2 or 4 or 6] and still more preferably at least 95% similarity (still more preferably at least 95% identity) to a polypeptide of Table 1 [SEQ ID NO:2 or 4 or 6] and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 30 amino acids and more preferably at least 50 amino acids.

20 The invention also includes polypeptides of the formula:



wherein, at the amino terminus, X is hydrogen, and at the carboxyl terminus, Y is hydrogen or a metal. R_1 and R_3 are any amino acid residue, m is an integer between 1 and 1000 or zero, n is an integer between 1 and 1000 or zero, and R_2 is an amino acid sequence of the invention,
 25 particularly an amino acid sequence selected from Table 1. In the formula above R_2 is oriented so that its amino terminal residue is at the left, bound to R_1 , and its carboxy terminal residue is at the right, bound to R_3 . Any stretch of amino acid residues denoted by either R group, where m and/or n is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.

30 A fragment is a variant polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the aforementioned polypeptides. As with FabD polypeptides fragments may be "free-standing," or comprised within a larger

polypeptide of which they form a part or region, most preferably as a single continuous region, a single larger polypeptide.

Preferred fragments include, for example, truncation polypeptides having a portion of an amino acid sequence of Table 1 [SEQ ID NO:2 or 4 or 6], or of variants thereof, such as a continuous series of residues that includes the amino terminus, or a continuous series of residues that includes the carboxyl terminus. Degradation forms of the polypeptides of the invention in a host cell, particularly a *Streptococcus pneumoniae*, are also preferred. Further preferred are fragments characterized by structural or functional attributes such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

Also preferred are biologically active fragments which are those fragments that mediate activities of FabD, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also included are those fragments that are antigenic or immunogenic in an animal, especially in a human. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *Streptococcus pneumoniae* or the ability to initiate, or maintain cause disease in an individual, particularly a human.

Variants that are fragments of the polypeptides of the invention may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be employed as intermediates for producing the full-length polypeptides of the invention.

In addition to the standard single and triple letter representations for amino acids, the term "X" or "Xaa" may also be used in describing certain polypeptides of the invention. "X" and "Xaa" mean any of the twenty naturally occurring amino acids may appear at such a designated position in the polypeptide sequence.

Polynucleotides

Another aspect of the invention relates to isolated polynucleotides, including the full length gene, that encode the FabD polypeptide having a deduced amino acid sequence of Table 1 [SEQ ID NO:2 or 4 or 6] and polynucleotides closely related thereto and variants thereof.

Using the information provided herein, such as a polynucleotide sequence set out in Table 1 [SEQ ID NO:1 or 3 or 5], a polynucleotide of the invention encoding FabD polypeptide may be obtained using standard cloning and screening methods, such as those for cloning and sequencing chromosomal DNA fragments from bacteria using *Streptococcus pneumoniae* 0100993 cells as starting material, followed by obtaining a full length clone. For example, to obtain a polynucleotide sequence of the invention, such as a sequence given in Table 1 [SEQ ID NO:1 or 3 or 5], typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae* 0100993 in *E.coli* or some other suitable host is probed with a radiolabeled oligonucleotide, preferably a 17-mer or longer, derived from a partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using stringent conditions. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently, such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989). (see in particular Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 13.70). Illustrative of the invention, the polynucleotide set out in Table 1 [SEQ ID NO:1 or 3 or 5] was discovered in a DNA library derived from *Streptococcus pneumoniae* 0100993.

The DNA sequence set out in Table 1 [SEQ ID NO:1 or 3 or 5] contains an open reading frame encoding a protein having about the number of amino acid residues set forth in Table 1 [SEQ ID NO:2 or 4 or 6] with a deduced molecular weight that can be calculated using amino acid residue molecular weight values well known in the art. The polynucleotide of SEQ ID NO: 1, between nucleotide number 1 and the stop codon underlined in Table 1(A) [SEQ ID NO:1], encodes the polypeptide of SEQ ID NO:2.

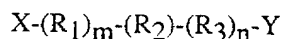
FabD of the invention is structurally related to other proteins of the malonyl-CoA:ACP family, as shown by the results of sequencing the DNA encoding FabD of the deposited strain.

The invention provides a polynucleotide sequence identical over its entire length to a coding sequence in Table 1 [SEQ ID NO:1 or 3 or 5]. Also provided by the invention is the coding sequence for the mature polypeptide or a fragment thereof, by itself as well as the coding sequence for the mature polypeptide or a fragment in reading frame with other coding

sequence, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro-protein sequence. The polynucleotide may also contain non-coding sequences, including for example, but not limited to non-coding 5' and 3' sequences, such as the transcribed, non-translated sequences, termination signals, ribosome binding sites, sequences that stabilize mRNA, introns, polyadenylation signals, and additional coding sequence which encode additional amino acids. For example, a marker sequence that facilitates purification of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, *Proc. Natl. Acad. Sci., USA* 86: 821-824 (1989), or an HA tag (Wilson *et al.*, *Cell* 37: 767 (1984). Polynucleotides of the invention also include, but are not limited to, polynucleotides comprising a structural gene and its naturally associated sequences that control gene expression.

A preferred embodiment of the invention is a polynucleotide of comprising nucleotide 1 to the nucleotide immediately upstream of the stop codon set forth in SEQ ID NO:1 of Table 1, both of which encode the FabD polypeptide.

The invention also includes polynucleotides of the formula:



wherein, at the 5' end of the molecule, X is hydrogen, and at the 3' end of the molecule, Y is hydrogen or a metal, R_1 and R_3 is any nucleic acid residue, m is an integer between 1 and 3000 or zero, n is an integer between 1 and 3000 or zero, and R_2 is a nucleic acid sequence of the invention, particularly a nucleic acid sequence selected from Table 1. In the polynucleotide formula above R_2 is oriented so that its 5' end residue is at the left, bound to R_1 , and its 3' end residue is at the right, bound to R_3 . Any stretch of nucleic acid residues denoted by either R group, where m and/or n is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer. In a preferred embodiment m and/or n is an integer between 1 and 1000.

It is most preferred that the polynucleotides of the inventions are derived from *Streptococcus pneumoniae*, however, they may preferably be obtained from organisms of the same taxonomic genus. They may also be obtained, for example, from organisms of the same taxonomic family or order.

The term "polynucleotide encoding a polypeptide" as used herein encompasses polynucleotides that include a sequence encoding a polypeptide of the invention, particularly a bacterial polypeptide and more particularly a polypeptide of the *Streptococcus pneumoniae*

FabD having an amino acid sequence set out in Table 1 [SEQ ID NO:2 or 4 or 6]. The term also encompasses polynucleotides that include a single continuous region or discontinuous regions encoding the polypeptide (for example, interrupted by integrated phage or an insertion sequence or editing) together with additional regions, that also may contain coding and/or non-coding sequences.

The invention further relates to variants of the polynucleotides described herein that encode for variants of the polypeptide having a deduced amino acid sequence of Table 1 [SEQ ID NO:2 or 4 or 6]. Variants that are fragments of the polynucleotides of the invention may be used to synthesize full-length polynucleotides of the invention.

Further particularly preferred embodiments are polynucleotides encoding FabD variants, that have the amino acid sequence of FabD polypeptide of Table 1 [SEQ ID NO:2 or 4 or 6] in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, that do not alter the properties and activities of FabD.

Further preferred embodiments of the invention are polynucleotides that are at least 70% identical over their entire length to a polynucleotide encoding FabD polypeptide having an amino acid sequence set out in Table 1 [SEQ ID NO:2 or 4 or 6], and polynucleotides that are complementary to such polynucleotides. Alternatively, most highly preferred are polynucleotides that comprise a region that is at least 80% identical over its entire length to a polynucleotide encoding FabD polypeptide of the deposited strain and polynucleotides complementary thereto. In this regard, polynucleotides at least 90% identical over their entire length to the same are particularly preferred, and among these particularly preferred polynucleotides, those with at least 95% are especially preferred. Furthermore, those with at least 97% are highly preferred among those with at least 95%, and among these those with at least 98% and at least 99% are particularly highly preferred, with at least 99% being the more preferred.

Preferred embodiments are polynucleotides that encode polypeptides that retain substantially the same biological function or activity as the mature polypeptide encoded by a DNA of Table 1 [SEQ ID NO:1 or 3 or 5].

The invention further relates to polynucleotides that hybridize to the herein above-described sequences. In this regard, the invention especially relates to polynucleotides that hybridize under stringent conditions to the herein above-described polynucleotides. As herein used, the terms "stringent conditions" and "stringent hybridization conditions" mean

hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. An example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual. Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

- 10 The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence set forth in SEQ ID NO:1 under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in SEQ ID NO:1 or a fragment thereof; and isolating said DNA sequence.
- 15 Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

- As discussed additionally herein regarding polynucleotide assays of the invention, for instance, polynucleotides of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding FabD and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the FabD gene. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 30 bases and may have at least 50 bases. Particularly preferred probes will have at least 30 bases and will have 50 bases or less.
- 20

- For example, the coding region of the FabD gene may be isolated by screening using a DNA sequence provided in Table 1 [SEQ ID NO: 1 or 3] to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine which members of the library the probe hybridizes to.
- 25

- The polynucleotides and polypeptides of the invention may be employed, for example, as research reagents and materials for discovery of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to polynucleotide assays.
- 30

Polynucleotides of the invention that are oligonucleotides derived from the sequences of Table 1 [SEQ ID NOS:1 or 2 or 3 or 4] may be used in the processes herein as described, but preferably for PCR, to determine whether or not the polynucleotides identified herein in whole or in part are transcribed in bacteria in infected tissue. It is
5 recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

The invention also provides polynucleotides that may encode a polypeptide that is the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature polypeptide (when the mature form has more than one polypeptide
10 chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, may allow protein transport, may lengthen or shorten protein half-life or may facilitate manipulation of a protein for assay or production, among other things. As generally is the case *in vivo*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

15 A precursor protein, having the mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. When prosequences are removed such inactive precursors generally are activated. Some or all of the prosequences may be removed before activation. Generally, such precursors are called proproteins.

In addition to the standard A, G, C, T/U representations for nucleic acid bases, the
20 term "N" may also be used in describing certain polynucleotides of the invention. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA sequence, except it is preferred that N is not a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

25 In sum, a polynucleotide of the invention may encode a mature protein, a mature protein plus a leader sequence (which may be referred to as a preprotein), a precursor of a mature protein having one or more prosequences that are not the leader sequences of a preprotein, or a preproprotein, which is a precursor to a proprotein, having a leader sequence and one or more prosequences, which generally are removed during processing steps that
30 produce active and mature forms of the polypeptide.

Vectors, host cells, expression

The invention also relates to vectors that comprise a polynucleotide or polynucleotides of the invention, host cells that are genetically engineered with vectors of the

invention and the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the invention.

For recombinant production, host cells can be genetically engineered to incorporate
5 expression systems or portions thereof or polynucleotides of the invention. Introduction of a polynucleotide into the host cell can be effected by methods described in many standard laboratory manuals, such as Davis et al., *BASIC METHODS IN MOLECULAR BIOLOGY*, (1986) and Sambrook et al., *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), such as, calcium
10 phosphate transfection, DEAE-dextran mediated transfection, transvection, microinjection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction and infection.

Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, enterococci *E. coli*, streptomyces and *Bacillus subtilis* cells;
15 fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used to produce the polypeptides of the invention. Such vectors include, among others, chromosomal, episomal and virus-derived
20 vectors, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and bacteriophage genetic
25 elements, such as cosmids and phagemids. The expression system constructs may contain control regions that regulate as well as engender expression. Generally, any system or vector suitable to maintain, propagate or express polynucleotides and/or to express a polypeptide in a host may be used for expression in this regard. The appropriate DNA sequence may be inserted into the expression system by any of a variety of well-known and routine techniques,
30 such as, for example, those set forth in Sambrook et al., *MOLECULAR CLONING, A LABORATORY MANUAL*, (*supra*).

For secretion of the translated protein into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals

may be incorporated into the expressed polypeptide. These signals may be endogenous to the polypeptide or they may be heterologous signals.

Polypeptides of the invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid
5 extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding protein may be employed to regenerate active conformation when the polypeptide is denatured during
10 isolation and or purification.

Diagnostic Assays

This invention is also related to the use of the FabD polynucleotides of the invention for use as diagnostic reagents. Detection of FabD in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes
15 (herein also "individual(s)"), particularly mammals, and especially humans, particularly those infected or suspected to be infected with an organism comprising the FabD gene may be detected at the nucleic acid level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly
20 for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA, cDNA and genomic DNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to
25 the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled FabD polynucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or
30 by direct DNA sequencing. See, e.g., Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques. to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to used RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan.

5 RNA, cDNA or genomic DNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding FabD can be used to identify and analyze mutations. These primers may be used for, among other things, amplifying FabD DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then

10 be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining

15 from a sample derived from an individual a increased level of expression of polynucleotide having a sequence of Table 1 [SEQ ID NO: 1 or 3]. Increased or decreased expression of FabD polynucleotide can be measured using any on of the methods well known in the art for the quantation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

20 In addition, a diagnostic assay in accordance with the invention for detecting over-expression of FabD protein compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a FabD protein, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays,

25 Western Blot analysis and ELISA assays.

Antibodies

The polypeptides of the invention or variants thereof, or cells expressing them can be used as an immunogen to produce antibodies immunospecific for such polypeptides. "Antibodies" as used herein includes monoclonal and polyclonal antibodies, chimeric, single

30 chain, simianized antibodies and humanized antibodies, as well as Fab fragments, including the products of an Fab immunoglobulin expression library.

Antibodies generated against the polypeptides of the invention can be obtained by administering the polypeptides or epitope-bearing fragments, analogues or cells to an animal,

preferably a nonhuman, using routine protocols. For preparation of monoclonal antibodies, any technique known in the art that provides antibodies produced by continuous cell line cultures can be used. Examples include various techniques, such as those in Kohler, G. and Milstein, C., *Nature* 256: 495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983);
5 Cole *et al.*, pg. 77-96 in *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc. (1985).

Techniques for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express
10 humanized antibodies.

Alternatively phage display technology may be utilized to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-FabD or from naive libraries (McCafferty, J. *et al.*, (1990), *Nature* 348, 552-554; Marks, J. *et al.*, (1992)
15 *Biotechnology* 10, 779-783). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. *et al.*, (1991) *Nature* 352, 624-628).

If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones
20 expressing the polypeptides to purify the polypeptides by affinity chromatography.

Thus, among others, antibodies against FabD- polypeptide may be employed to treat infections, particularly bacterial infections.

Polypeptide variants include antigenically, epitopically or immunologically equivalent variants that form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a polypeptide or its equivalent which
25 will be specifically recognized by certain antibodies which, when raised to the protein or polypeptide according to the invention, interfere with the immediate physical interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable
30 formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the immediate physical interaction between pathogen and mammalian host.

The polypeptide, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such

as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughput screening assays to identify antagonists. See, D. Bennett *et al.*, *Journal of Molecular Recognition*, Vol. 8 52-58 (1995) and K. Johanson *et al.*, *The Journal of Biological Chemistry*, Vol. 270, No. 16, pp 9459-9471 (1995).

Preferably, the antibody or variant thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized"; where the complementarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. *et al.* (1986), *Nature* 321, 522-525 or Tempest *et al.*, (1991) *Biotechnology* 9, 266-273.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, *Hum Mol Genet* 1992, 1:363, Manthorpe *et al.*, *Hum. Gene Ther.* 1993:4, 419), delivery of DNA complexed with specific protein carriers (Wu *et al.*, *J Biol Chem.* 1989: 264,16985), coprecipitation of DNA with calcium phosphate (Benvenisty & Reshef, *PNAS USA*, 1986:83,9551), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, *Science* 1989:243,375), particle bombardment (Tang *et al.*, *Nature* 1992, 356:152, Eisenbraun *et al.*, *DNA Cell Biol* 1993, 12:791) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, *PNAS USA* 1984:81,5849).

30 Antagonists and agonists - assays and molecules

Polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates

and ligands or may be structural or functional mimetics. See, *e.g.*, Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

5 The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of FabD polypeptides or polynucleotides, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising FabD polypeptide and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be a FabD agonist or antagonist. The ability of the candidate molecule to agonize or antagonize the FabD polypeptide is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, *i.e.*, without inducing the effects of FabD polypeptide are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in FabD polynucleotide or polypeptide activity, and binding assays known in the art.

20 Another example of an assay for FabD antagonists is a competitive assay that combines FabD and a potential antagonist with FabD-binding molecules, recombinant FabD binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. FabD can be labeled, such as by radioactivity or a colorimetric compound, such that the number of FabD molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

30 Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, such as a binding molecule, without inducing FabD-induced activities, thereby preventing the action of FabD by excluding FabD from binding.

Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of FabD.

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block FabD protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial FabD proteins that mediate tissue damage and; to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat diseases.

Helicobacter pylori (herein *H. pylori*) bacteria infect the stomachs of over one-third of the world's population causing stomach cancer, ulcers, and gastritis (International Agency for Research on Cancer (1994) Schistosomes, Liver Flukes and *Helicobacter Pylori* (International Agency for Research on Cancer, Lyon, France; <http://www.uicc.ch/ecp/ecp2904.htm>). Moreover, the international Agency for Research on Cancer recently recognized a cause-and-effect relationship between *H. pylori* and gastric

adenocarcinoma, classifying the bacterium as a Group I (definite) carcinogen. Preferred antimicrobial compounds of the invention (agonists and antagonists of FabD) found using screens provided by the invention, particularly broad-spectrum antibiotics, should be useful in the treatment of *H. pylori* infection. Such treatment should decrease the advent of *H. pylori*-induced cancers, such as gastrointestinal carcinoma. Such treatment should also cure gastric ulcers and gastritis.

Vaccines

Another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal which comprises inoculating the individual with FabD, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said individual from infection, particularly bacterial infection and most particularly *Streptococcus pneumoniae* infection. Also provided are methods whereby such immunological response slows bacterial replication. Yet another aspect of the invention relates to a method of inducing immunological response in an individual which comprises delivering to such individual a nucleic acid vector to direct expression of FabD, or a fragment or a variant thereof, for expressing FabD, or a fragment or a variant thereof *in vivo* in order to induce an immunological response, such as, to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid.

A further aspect of the invention relates to an immunological composition which, when introduced into an individual capable or having induced within it an immunological response, induces an immunological response in such individual to a FabD or protein coded therefrom, wherein the composition comprises a recombinant FabD or protein coded therefrom comprising DNA which codes for and expresses an antigen of said FabD or protein coded therefrom. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

A FabD polypeptide or a fragment thereof may be fused with co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing

a fused protein which will have immunogenic and protective properties. Thus fused recombinant protein, preferably further comprises an antigenic co-protein, such as lipoprotein D from *Hemophilus influenzae*, Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilize the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Provided by this invention are compositions, particularly vaccine compositions, and methods comprising the polypeptides or polynucleotides of the invention and immunostimulatory DNA sequences, such as those described in Sato, Y. *et al.* Science 273: 352 (1996).

Also, provided by this invention are methods using the described polynucleotide or particular fragments thereof which have been shown to encode non-variable regions of bacterial cell surface proteins in DNA constructs used in such genetic immunization experiments in animal models of infection with *Streptococcus pneumoniae* will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. It is believed that this approach will allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of bacterial infection, particularly *Streptococcus pneumoniae* infection, in mammals, particularly humans.

The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue caused, e.g., by mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The invention also includes a vaccine formulation which comprises an immunogenic recombinant protein of the invention together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, or intradermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats

and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials and may be
5 stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

10 While the invention has been described with reference to certain FabD protein, it is to be understood that this covers fragments of the naturally occurring protein and similar proteins with additions, deletions or substitutions which do not substantially affect the immunogenic properties of the recombinant protein.

Compositions, kits and administration

15 The invention also relates to compositions comprising the polynucleotide or the polypeptides discussed above or their agonists or antagonists. The polypeptides of the invention may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a
20 therapeutically effective amount of a polypeptide of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration. The invention further relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of
25 the ingredients of the aforementioned compositions of the invention.

Polypeptides and other compounds of the invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous,
30 intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to mammals, and particularly humans, it is expected that the daily dosage level of the active agent will be from 0.01 mg/kg to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual and will vary with the age, weight and response of the particular individual. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this invention.

In-dwelling devices include surgical implants, prosthetic devices and catheters, i.e., devices that are introduced to the body of an individual and remain in position for an extended time. Such devices include, for example, artificial joints, heart valves, pacemakers, vascular grafts, vascular catheters, cerebrospinal fluid shunts, urinary catheters, continuous ambulatory peritoneal dialysis (CAPD) catheters.

The composition of the invention may be administered by injection to achieve a systemic effect against relevant bacteria shortly before insertion of an in-dwelling device. Treatment may be continued after surgery during the in-body time of the device. In addition, the composition could also be used to broaden perioperative cover for any surgical technique to prevent bacterial wound infections, especially *Streptococcus pneumoniae* wound infections.

Many orthopaedic surgeons consider that humans with prosthetic joints should be considered for antibiotic prophylaxis before dental treatment that could produce a bacteremia. Late deep infection is a serious complication sometimes leading to loss of the prosthetic joint and is accompanied by significant morbidity and mortality. It may therefore be possible to extend the use of the active agent as a replacement for prophylactic antibiotics in this situation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

5 Alternatively, the composition of the invention may be used to bathe an indwelling device immediately before insertion. The active agent will preferably be present at a concentration of 1µg/ml to 10mg/ml for bathing of wounds or indwelling devices.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 10 0.5-5 microgram/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks. With the indicated dose range, no adverse toxicological effects will be observed with the compounds of the invention which would preclude their administration to suitable individuals.

Each reference disclosed herein is incorporated by reference herein in its entirety.
15 Any patent application to which this application claims priority is also incorporated by reference herein in its entirety.

GLOSSARY

The following definitions are provided to facilitate understanding of certain terms used frequently herein.

20 "Disease(s)" means and disease caused by or related to infection by a bacteria, including otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

"Host cell" is a cell which has been transformed or transfected, or is capable of 25 transformation or transfection by an exogenous polynucleotide sequence.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match 30 between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993;

- Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)). As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence of SEQ ID NO: 1 it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence of SEQ ID NO: 1. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Analogously, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of SEQ ID NO:2 is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid of SEQ ID NO: 2. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number

of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues
5 in the reference sequence or in one or more contiguous groups within the reference sequence.

"Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not
10 "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotide(s)" include, without limitation, single- and double-stranded DNA, DNA that
15 is a mixture of single- and double-stranded regions or single-, double- and triple-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded regions, or a mixture of single- and double-stranded regions. In addition, "polynucleotide" as used herein refers to triple-stranded regions
20 comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term "polynucleotide(s)" also includes DNAs or RNAs as described above that contain one or more
25 modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotide(s)" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful
30 purposes known to those of skill in the art. The term "polynucleotide(s)" as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and

cells, including, for example, simple and complex cells. "Polynucleotide(s)" also embraces short polynucleotides often referred to as oligonucleotide(s).

"Polypeptide(s)" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds. "Polypeptide(s)" refers to both short chains, commonly referred to as peptides, oligopeptides and oligomers and to longer chains generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene encoded amino acids. "Polypeptide(s)" include those modified either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains, and the amino or carboxyl termini. Modifications include, for example, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins, such as arginylation, and ubiquitination. See, for instance, *PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993) and Wold, F., *Posttranslational Protein Modifications: Perspectives and Prospects*, pgs. 1-12 in *POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter et al., *Meth. Enzymol.* 182:626-646 (1990) and Rattan et al., *Protein Synthesis: Posttranslational Modifications and Aging*, Ann. N.Y. Acad. Sci. 663: 48-62 (1992). Polypeptides may be branched or cyclic, with or without branching. Cyclic, branched and

branched circular polypeptides may result from post-translational natural processes and may be made by entirely synthetic methods, as well.

“Variant(s)” as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques, by direct synthesis, and by other recombinant methods known to skilled artisans.

20 EXAMPLES

The examples below are carried out using standard techniques, which are well known and routine to those of skill in the art, except where otherwise described in detail. The examples are illustrative, but do not limit the invention.

Example 1 Strain selection, Library Production and Sequencing

25 The polynucleotide having a DNA sequence given in Table 1 [SEQ ID NO:1 or 3 or 5] was obtained from a library of clones of chromosomal DNA of *Streptococcus pneumoniae* in *E. coli*. The sequencing data from two or more clones containing overlapping *Streptococcus pneumoniae* DNAs was used to construct the contiguous DNA sequence in SEQ ID NO:1. Libraries may be prepared by routine methods, for example:
30 Methods 1 and 2 below.

Total cellular DNA is isolated from *Streptococcus pneumoniae* 0100993 according to standard procedures and size-fractionated by either of two methods.

Method 1

Total cellular DNA is mechanically sheared by passage through a needle in order to size-fractionate according to standard procedures. DNA fragments of up to 11kbp in size are rendered blunt by treatment with exonuclease and DNA polymerase, and EcoRI linkers added. Fragments are ligated into the vector Lambda ZapII that has been cut with EcoRI, the library packaged by standard procedures and *E.coli* infected with the packaged library. The library is amplified by standard procedures.

Method 2

Total cellular DNA is partially hydrolyzed with a one or a combination of restriction enzymes appropriate to generate a series of fragments for cloning into library vectors (e.g., RsaI, PstI, AluI, BshI235I), and such fragments are size-fractionated according to standard procedures. EcoRI linkers are ligated to the DNA and the fragments then ligated into the vector Lambda ZapII that have been cut with EcoRI, the library packaged by standard procedures, and *E.coli* infected with the packaged library. The library is amplified by standard procedures.

Example 2 FabD Characterization

FabD malonyl-CoA:ACP transacylase activity can be readily assayed *via* the incorporation of ^{14}C -malonate from trichloroacetic acid soluble ^{14}C -malonyl-CoA into TCA insoluble ^{14}C -malonyl-ACP, using ACP as acceptor. Test compounds may be added to this assay to determine whether they agonise or antagonise enzyme activity.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Gentry, Daniel

Lonsdale, John

Payne, David

Pearson, Stewart

Van Aller, Glenn

(ii) TITLE OF THE INVENTION: Novel FabD

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation

(B) STREET: 709 Swedeland Road

(C) CITY: King of Prussia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 14-NOV-1997

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/031,160

(B) FILING DATE: 18-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Gimmi, Edward R
- (B) REGISTRATION NUMBER: 38,891
- (C) REFERENCE/DOCKET NUMBER: P50593

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGACTAAAA CAGCCTTTTT ATTTGCTGGT CAAGGTGCCC AGTATCTAGG GATGGGACGG      60
GATTTCTATG ATCAGTATCC GATTGTCAAA GAAACGATTG ATCGAGCGAG TCAGGTGCTC      120
GGTTATGATT TACGTTATCT CATCGATACG GAAGAAGACA AACTCAATCA GACCCGCTAT      180
ACGCAACCAG CCATTCTAGC GACTTCGGTT GCTATCTACC GTTTATTGCA AGAAAAGGGC      240
TATCAGCCTG ATATGGTTGC TGGTTTGTCT CTTGGAGAAT ACTCTGCCTT GGTGGCAAGC      300
GGCGCCTTGG ATTTTGAAGA TCGGTTGCC TTGGTAGCTA AGCGTGGAGC CTATATGGAA      360
GAAGCGGCTC CTGCTGACTC TGGCAAGATG GTAGCAGTTC TCAATACGCC AGTAGAGGTC      420
ATTGAAGAAG CCTGTCAAAA AGCTTCTGAA CTTGGAGTGG TTAATCCAGC CAACTATAAC      480
ACACCTGCAC AAATCGTCAT TGCTGGAGAA GTGGTTGCAG TTGATCGAGC GGTTGAACTT      540
TTGCAAGAAG CAGGTGCCAA ACGCTTGATT CCTCTTAAGG TGTCAGGTCC CTTTCACACC      600
GCTCTCCTTG AGCCTGCTAG CCAGAAACTA GCTGAACTC TAGCTCAGGT AAGTTTTTCA      660
GATTTTACTT GTCCCCTAGT CGGCAATACA GAAGCTGCTG TGATGCAAAA AGAGGACATT      720
GCTCAGCTCT TGACGCGTCA GGTCAAGGAA CCCGTTCTGT TCTATGAAAG TATTGGGGTC      780
ATGCAAGAAG CAGGCATAAG CAACTTTATC GAGATTGGAC CGGGGAAAGT CTTGTCAGGT      840

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TTTGTAAAA AAATTGATCA AACTGCTCAC TTAGCTCATG TGGAAGATCA AGCGAGTTTA 900
GTAGCACTTT TAGAAAAATA G 921

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Lys	Thr	Ala	Phe	Leu	Phe	Ala	Gly	Gln	Gly	Ala	Gln	Tyr	Leu
1				5					10					15	
Gly	Met	Gly	Arg	Asp	Phe	Tyr	Asp	Gln	Tyr	Pro	Ile	Val	Lys	Glu	Thr
			20					25					30		
Ile	Asp	Arg	Ala	Ser	Gln	Val	Leu	Gly	Tyr	Asp	Leu	Arg	Tyr	Leu	Ile
	35					40					45				
Asp	Thr	Glu	Glu	Asp	Lys	Leu	Asn	Gln	Thr	Arg	Tyr	Thr	Gln	Pro	Ala
	50				55					60					
Ile	Leu	Ala	Thr	Ser	Val	Ala	Ile	Tyr	Arg	Leu	Leu	Gln	Glu	Lys	Gly
65				70					75					80	
Tyr	Gln	Pro	Asp	Met	Val	Ala	Gly	Leu	Ser	Leu	Gly	Glu	Tyr	Ser	Ala
			85					90					95		
Leu	Val	Ala	Ser	Gly	Ala	Leu	Asp	Phe	Glu	Asp	Ala	Val	Ala	Leu	Val
	100					105						110			
Ala	Lys	Arg	Gly	Ala	Tyr	Met	Glu	Glu	Ala	Ala	Pro	Ala	Asp	Ser	Gly
	115					120					125				
Lys	Met	Val	Ala	Val	Leu	Asn	Thr	Pro	Val	Glu	Val	Ile	Glu	Glu	Ala
	130				135						140				
Cys	Gln	Lys	Ala	Ser	Glu	Leu	Gly	Val	Val	Thr	Pro	Ala	Asn	Tyr	Asn
145				150						155				160	
Thr	Pro	Ala	Gln	Ile	Val	Ile	Ala	Gly	Glu	Val	Val	Ala	Val	Asp	Arg
			165						170					175	

Ala Val Glu Leu Leu Gln Glu Ala Gly Ala Lys Arg Leu Ile Pro Leu
 180 185 190
 Lys Val Ser Gly Pro Phe His Thr Ala Leu Leu Glu Pro Ala Ser Gln
 195 200 205
 Lys Leu Ala Glu Thr Leu Ala Gln Val Ser Phe Ser Asp Phe Thr Cys
 210 215 220
 Pro Leu Val Gly Asn Thr Glu Ala Ala Val Met Gln Lys Glu Asp Ile
 225 230 235 240
 Ala Gln Leu Leu Thr Arg Gln Val Lys Glu Pro Val Arg Phe Tyr Glu
 245 250 255
 Ser Ile Gly Val Met Gln Glu Ala Gly Ile Ser Asn Phe Ile Glu Ile
 260 265 270
 Gly Pro Gly Lys Val Leu Ser Gly Phe Val Lys Lys Ile Asp Gln Thr
 275 280 285
 Ala His Leu Ala His Val Glu Asp Gln Ala Ser Leu Val Ala Leu Leu
 290 295 300
 Glu Lys
 305

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGAAGAAAT CCTAAAAGAT TTGTATTACG GAGCCGCTAA GAAAATTCAA GAAGAAGCCT	60
CTCGCTGGGC AGGAGTTGTA AGAAATGACT AAAACAGCCT TTTTATTTGC TGGTCAAGGT	120
GCCCAGTATC TAGGGATGGG ACGGGATTTT TATGATCAGT ATCCGATTGT CAAAGAAACG	180
ATTGATCGAG CGAGTCAGGT GCTCGGTTAT GATTTACGTT ATCTCATCGA TACGGAAGAA	240
GACAAACTCA ATCAGACCCG CTATACGCAA CCAGCCATTC TAGCGACTTC GGTGCTATC	300
TACCGTTTAT TGCAAGAAAA GGGCTATCAG CCTGATATGG TTGCTGGTTT GTCTCTTGA	360

GAATACTCTG CCTTGGTGGC AAGCGGCGCC TTGGATTTTG AAGATGCGGT TGCCTTGGTA 420
GCTAAGCGTG GAGCCTATAT GGAAGAAGCG 450

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Lys Thr Ala Phe Leu Phe Ala Gly Gln Gly Ala Gln Tyr Leu
1 5 10 15
Gly Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr
20 25 30
Ile Asp Arg Ala Ser Gln Val Leu Gly Tyr Asp Leu Arg Tyr Leu Ile
35 40 45
Asp Thr Glu Glu Asp Lys Leu Asn Gln Thr Arg Tyr Thr Gln Pro Ala
50 55 60
Ile Leu Ala Thr Ser Val Ala Ile Tyr Arg Leu Leu Gln Glu Lys Gly
65 70 75 80
Tyr Gln Pro Asp Met Val Ala Gly Leu Ser Leu Gly Glu Tyr Ser Ala
85 90 95
Leu Val Ala Ser Gly Ala Leu Asp Phe Glu Asp Ala Val Ala Leu Val
100 105 110
Ala Lys Arg Gly Ala Tyr Met Glu Glu Ala
115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCTGAACTT GGCAAGATGG TAGCAGTTCT CAATACGCCA GTAGAGGTCA TTGAAGAAGC	60
CTGTCAAAAG CTTCTGGAAC TTGGAGTGGT TACTCCAGCC AACTATAACA CACCTGCACA	120
AATCGTCATT GCTGGAGAAG TGGTTGCAGT TGATCGAGCG GTTGAAC TTT TGCAAGAAGC	180
AGGTGCCAAA CGCTTGATTC CTCTTAAGGT GTCAGGTCCC TTTCACACCG CTCTCCTTGA	240
GCCTGCTAGC CAGAACTAG CTGAACTCT AGCTCAGGTA AGTTTTTCAG ATTTTACTTG	300
TCCCCTAGTC GGCAATACAG AAGCTGCTGT GATGCAAAAA GAGGACATTG CTCAGCTCTT	360
GACGCGTCAG GTCAAGGAAC CCGTTCGTTT CTATGAAAGT ATTGGGGTCA TGCAAGAAGC	420
AGGCATAAGC AACTTATTCG AGATTGGACC GGGGAAAGTC TTGTCAGGTT TTGTTAAAAA	480
AATTGATCAA ACTGCTCACT TAGCTCATGT GGAAGATCAA GCGAGTTTAG TAGCACTTTT	540
AGAAAAA	547

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala	Glu	Leu	Gly	Lys	Met	Val	Ala	Val	Leu	Asn	Thr	Pro	Val	Glu	Val
1				5					10					15	
Ile	Glu	Glu	Ala	Cys	Gln	Lys	Leu	Leu	Glu	Leu	Gly	Val	Val	Thr	Pro
			20						25					30	
Ala	Asn	Tyr	Asn	Thr	Pro	Ala	Gln	Ile	Val	Ile	Ala	Gly	Glu	Val	Val
			35						40					45	

Ala Val Asp Arg Ala Val Glu Leu Leu Gln Glu Ala Gly Ala Lys Arg
 50 55 60
 Leu Ile Pro Leu Lys Val Ser Gly Pro Phe His Thr Ala Leu Leu Glu
 65 70 75 80
 Pro Ala Ser Gln Lys Leu Ala Glu Thr Leu Ala Gln Val Ser Phe Ser
 85 90 95
 Asp Phe Thr Cys Pro Leu Val Gly Asn Thr Glu Ala Ala Val Met Gln
 100 105 110
 Lys Glu Asp Ile Ala Gln Leu Leu Thr Arg Gln Val Lys Glu Pro Val
 115 120 125
 Arg Phe Tyr Glu Ser Ile Gly Val Met Gln Glu Ala Gly Ile Ser Asn
 130 135 140
 Leu Phe Glu Ile Gly Pro Gly Lys Val Leu Ser Gly Phe Val Lys Lys
 145 150 155 160
 Ile Asp Gln Thr Ala His Leu Ala His Val Glu Asp Gln Ala Ser Leu
 165 170 175
 Val Ala Leu Leu Glu Lys
 180

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What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2.
- 5 2. An isolated polynucleotide comprising a polynucleotide having at least a 70% identity to a polynucleotide encoding the same mature polypeptide expressed by the FabD gene contained in the *Streptococcus pneumoniae* of the deposited strain.
3. An isolated polynucleotide comprising a polynucleotide encoding a polypeptide comprising an amino acid sequence which is at least 70% identical to the amino
10 acid sequence of SEQ ID NO:2.
4. An isolated polynucleotide that is complementary to the polynucleotide of claim 1
5. The polynucleotide of Claim 1 wherein the polynucleotide is DNA or RNA
6. The polynucleotide of Claim 1 comprising the nucleic acid sequence set forth
15 in SEQ ID NO:1.
7. The polynucleotide of Claim 1 comprising nucleotide 1 to the stop codon set forth in SEQ ID NO:1.
8. The polynucleotide of Claim 1 which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.
- 20 9. A vector comprising the polynucleotide of Claim 1.
10. A host cell comprising the vector of Claim 9.
11. A process for producing a polypeptide comprising: expressing from the host cell of Claim 10 a polypeptide encoded by said DNA.
12. A process for producing a FabD polypeptide or fragment comprising
25 culturing a host of claim 10 under conditions sufficient for the production of said polypeptide or fragment.
13. A polypeptide comprising an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2.
14. A polypeptide comprising an amino acid sequence as set forth in SEQ ID
30 NO:2.
15. An antibody against the polypeptide of claim 14.
16. An antagonist which inhibits the activity or expression of the polypeptide of claim 14.

17. A method for the treatment of an individual in need of FabD polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 14.

5 18. A method for the treatment of an individual having need to inhibit FabD polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.

19. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 14 in an individual comprising:

- 10 (a) determining a nucleic acid sequence encoding said polypeptide, and/or
(b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.

20. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 14 comprising:

15 contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of providing a detectable signal in response to the interaction of the polypeptide with the compound;

20 and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.

21. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with FabD polypeptide of claim 14, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said
25 animal from disease.

22. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of FabD polypeptide of claim 14, or fragment or a variant thereof, for expressing said FabD polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody
30 and/ or T cell immune response to protect said animal from disease.

23. An isolated polynucleotide comprising a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:4.

24. An isolated polynucleotide comprising a polynucleotide having at least a 70% identity to the polynucleotide sequence of SEQ ID NO:3.

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DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

"Novel FabD"

the specification of which (check one)

☐ is attached hereto.

☒ was filed on **14 November 1997** as Serial No. **PCT/US97/20992**
and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or Inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Number	Country	Filing Date	Priority Claimed
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I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any United States provisional application(s) listed below.

Application Number	Filing Date
60/031,160	18 November 1996

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

Serial No.	Filing Date	Status
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I hereby appoint the practitioners associated with the Customer Number provided below to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith, and direct that all correspondence be addressed to that Customer Number:

Customer Number 20462.

Address all correspondence and telephone calls to Edward R. Gimmi, SmithKline Beecham Corporation, Corporate Intellectual Property-U.S., UW2220, P.O. Box 1539, King of Prussia, Pennsylvania 19406-0939, whose telephone number is 610-270-5017.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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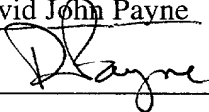
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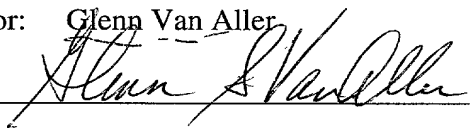
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